

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/588,030
Source: IFWP
Date Processed by STIC: 8/10/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/588,030

CRF Edit Date: 8/10/06
Edited by: [Signature]

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

/ Deleted: / invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

___ Other:



IFWP

RAW SEQUENCE LISTING

DATE: 08/10/2006

PATENT APPLICATION: US/10/588,030

TIME: 20:03:19

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08102006\J588030.raw

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3 <110> APPLICANT: Bayer HealthCare AG
5 <120> TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
6   Phosphate Regulating Endopeptidase Homolog (PHEX)
8 <130> FILE REFERENCE: 004974.01208
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/588,030
C--> 10 <141> CURRENT FILING DATE: 2006-08-01
10 <160> NUMBER OF SEQ ID NOS: 5
12 <170> SOFTWARE: PatentIn version 3.2
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 2590
16 <212> TYPE: DNA
17 <213> ORGANISM: Homo sapiens
19 <400> SEQUENCE: 1
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21 ctctacggcc cttctgatgg aagcagaaac agggagcagc gtggagactg gaaagaaggc      120
22 caacagaggc actcgaattg ccctggctcg gtttgctcgg ggcaccctag ttctgggcac      180
23 gatcctcttt ctagtgaagc aaggtctctt aagtctccaa gctaaacagg agtactgcct      240
24 gaagccagaa tgcacgaagc cggctgctgc catcttaagt aaagtaaata tgtctgtgga      300
25 tccttgtgat aatttcttcc ggttcgcttg tgatggctgg ataagcaata atccaattcc      360
26 cgaagatatg ccaagctatg gggtttatcc ttggctgaga cataatgttg acctcaagtt      420
27 gaaggaactt ttggagaaat caatcagtag aaggcgggac accgaagcca tacagaaagc      480
28 caaaatcctt tattcatcct gcatgaatga gaaagcgatt gaaaaagcag atgccaagcc      540
29 actgctacac atcctacggc attcaccttt ccgctggccc gtgcttgaat ctaatatgtg      600
30 ccctgaaggg gtttggtcag agagaaagtt cagccttctg cagacacttg caacgtttcg      660
31 tgggtcaatac agcaattctg tgttcacccg tttgtatgtg tccctgatg acaaagcatc      720
32 caatgaacat atcttgaagc tggaccaagc aacactctcc ctggccgtga ggggaagacta      780
33 ccttgataac agtacagaag ccaagtctta tcgggatgcc ctttacaagt tcatggtgga      840
34 tactgccgtg cttttaggag ctaacagttc cagagcagag catgacatga agtcagtgtc      900
35 cagattggaa attaagatag ctgagataat gattccacat gaaaaccgaa ccagcgaggc      960
36 catgtacaac aaaatgaaca tttctgaact gagtgctatg attccccagt tcgactggct      1020
37 gggctacatc aagaaggtea ttgacaccag actctacccc catctgaaag acatcagccc      1080
38 ctccgagaat gtggtggtcc gcgtcccgcg gtactttaaa gatttgttta ggatattagg      1140
39 gtctgagaga aagaagacca ttgccaaacta tttggtgtgg agaatggttt attccagaat      1200
40 tccaaacctt agcaggcgct ttcagtatag atggctggaa ttctcaaggg taatccaggg      1260
41 gaccacaact ttgctgcctc aatgggacaa atgtgtaaac tttattgaaa gtgccctccc      1320
42 ttatgttggt ggaaagatgt ttgtagatgt gtacttccag gaagataaga aggaaatgat      1380
43 ggaggaattg gttgagggcg ttcgctgggc ctttattgac atgctagaga aagaaaatga      1440
44 gtggatggat gcaggaacga aaaggaaaag caaagaaaag gcgagagctg ttttggcaaa      1500
45 agttggctat ccagagttta taatgaatga tactcatgtt aatgaagacc tcaaagctat      1560
46 caagttttca gaagccgact actttggcaa cgctctacaa actcgcaagt atttagcaca      1620
47 gtctgatttc ttctggctaa gaaaagccgt tccaaaaaca gagtggttta caaatccgac      1680
48 gactgtcaat gccttctaca gtgcatccac caaccagatc cgatttccag caggagagct      1740
49 ccagaagcct ttcttttggg gaacagaata tcctcgatct ctgagttatg gtgctatagg      1800

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PATENT APPLICATION: US/10/588,030

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50 agtaattgtc ggacatgaat ttacacatgg atttgataat aatggtagaa aatatgataa 1860
51 aaatggaaac ctggatcctt ggtggtctac tgaatcagaa gaaaagttaa aggaaaaaac 1920
52 aaaatgcatg attaaccagt atagcaacta ttattggaag aaagctggct taaatgtcaa 1980
53 ggggaagagg accctgggag aaaatattgc tgataatgga ggcctgcggg aagcttttag 2040
54 ggcttacagg aaatggataa atgacagaag gcagggactt gaggagcctc ttctaccagg 2100
55 catcacattc accaacaacc agctcttctt cctgagttat gctcatgtga ggtgcaattc 2160
56 ctacagacca gaagctgccc gagaacaagt ccaaattggg gctcacagtc cccctcagtt 2220
57 taggggtcaat ggtgcaatta gtaactttga agaattccag aaagctttta actgtccacc 2280
58 caattccacg atgaacagag gcatggactc ctgccgactc tggtagctgg gacgctgggt 2340
59 tatggcatcc tgagacagtt gcacagtgcc agcggaggct gcactgagcc ttcacgccc 2400
60 attgcttttag gctggagac tticattttt agtgcatttt cattatttgg gtaggtgacc 2460
61 tgcttgatc tagacagcat ctgttcaaag tcgtagggct tataaagtgg aatataagaa 2520
62 tgaactaagt atgtttcttt agaaaatcaa accaacaaaa ataaatccct aggctacttt 2580
63 tgtaaaaaaa 2590

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65 <210> SEQ ID NO: 2

66 <211> LENGTH: 749

67 <212> TYPE: PRT

68 <213> ORGANISM: Homo sapiens

70 <400> SEQUENCE: 2

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71 Met Glu Ala Glu Thr Gly Ser Ser Val Glu Thr Gly Lys Lys Ala Asn
72 1 5 10 15
73 Arg Gly Thr Arg Ile Ala Leu Val Val Phe Val Gly Gly Thr Leu Val
74 20 25 30
75 Leu Gly Thr Ile Leu Phe Leu Val Ser Gln Gly Leu Leu Ser Leu Gln
76 35 40 45
77 Ala Lys Gln Glu Tyr Cys Leu Lys Pro Glu Cys Ile Glu Ala Ala Ala
78 50 55 60
79 Ala Ile Leu Ser Lys Val Asn Leu Ser Val Asp Pro Cys Asp Asn Phe
80 65 70 75 80
81 Phe Arg Phe Ala Cys Asp Gly Trp Ile Ser Asn Asn Pro Ile Pro Glu
82 85 90 95
83 Asp Met Pro Ser Tyr Gly Val Tyr Pro Trp Leu Arg His Asn Val Asp
84 100 105 110
85 Leu Lys Leu Lys Glu Leu Leu Glu Lys Ser Ile Ser Arg Arg Arg Asp
86 115 120 125
87 Thr Glu Ala Ile Gln Lys Ala Lys Ile Leu Tyr Ser Ser Cys Met Asn
88 130 135 140
89 Glu Lys Ala Ile Glu Lys Ala Asp Ala Lys Pro Leu Leu His Ile Leu
90 145 150 155 160
91 Arg His Ser Pro Phe Arg Trp Pro Val Leu Glu Ser Asn Ile Gly Pro
92 165 170 175
93 Glu Gly Val Trp Ser Glu Arg Lys Phe Ser Leu Leu Gln Thr Leu Ala
94 180 185 190
95 Thr Phe Arg Gly Gln Tyr Ser Asn Ser Val Phe Ile Arg Leu Tyr Val
96 195 200 205
97 Ser Pro Asp Asp Lys Ala Ser Asn Glu His Ile Leu Lys Leu Asp Gln
98 210 215 220
99 Ala Thr Leu Ser Leu Ala Val Arg Glu Asp Tyr Leu Asp Asn Ser Thr
100 225 230 235 240

```

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08102006\J588030.raw

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101 Glu Ala Lys Ser Tyr Arg Asp Ala Leu Tyr Lys Phe Met Val Asp Thr
102          245          250          255
103 Ala Val Leu Leu Gly Ala Asn Ser Ser Arg Ala Glu His Asp Met Lys
104          260          265          270
105 Ser Val Leu Arg Leu Glu Ile Lys Ile Ala Glu Ile Met Ile Pro His
106          275          280          285
107 Glu Asn Arg Thr Ser Glu Ala Met Tyr Asn Lys Met Asn Ile Ser Glu
108          290          295          300
109 Leu Ser Ala Met Ile Pro Gln Phe Asp Trp Leu Gly Tyr Ile Lys Lys
110          305          310          315          320
111 Val Ile Asp Thr Arg Leu Tyr Pro His Leu Lys Asp Ile Ser Pro Ser
112          325          330          335
113 Glu Asn Val Val Val Arg Val Pro Gln Tyr Phe Lys Asp Leu Phe Arg
114          340          345          350
115 Ile Leu Gly Ser Glu Arg Lys Lys Thr Ile Ala Asn Tyr Leu Val Trp
116          355          360          365
117 Arg Met Val Tyr Ser Arg Ile Pro Asn Leu Ser Arg Arg Phe Gln Tyr
118          370          375          380
119 Arg Trp Leu Glu Phe Ser Arg Val Ile Gln Gly Thr Thr Thr Leu Leu
120          385          390          395          400
121 Pro Gln Trp Asp Lys Cys Val Asn Phe Ile Glu Ser Ala Leu Pro Tyr
122          405          410          415
123 Val Val Gly Lys Met Phe Val Asp Val Tyr Phe Gln Glu Asp Lys Lys
124          420          425          430
125 Glu Met Met Glu Glu Leu Val Glu Gly Val Arg Trp Ala Phe Ile Asp
126          435          440          445
127 Met Leu Glu Lys Glu Asn Glu Trp Met Asp Ala Gly Thr Lys Arg Lys
128          450          455          460
129 Ala Lys Glu Lys Ala Arg Ala Val Leu Ala Lys Val Gly Tyr Pro Glu
130          465          470          475          480
131 Phe Ile Met Asn Asp Thr His Val Asn Glu Asp Leu Lys Ala Ile Lys
132          485          490          495
133 Phe Ser Glu Ala Asp Tyr Phe Gly Asn Val Leu Gln Thr Arg Lys Tyr
134          500          505          510
136 Leu Ala Gln Ser Asp Phe Phe Trp Leu Arg Lys Ala Val Pro Lys Thr
137          515          520          525
138 Glu Trp Phe Thr Asn Pro Thr Thr Val Asn Ala Phe Tyr Ser Ala Ser
139          530          535          540
140 Thr Asn Gln Ile Arg Phe Pro Ala Gly Glu Leu Gln Lys Pro Phe Phe
141          545          550          555          560
142 Trp Gly Thr Glu Tyr Pro Arg Ser Leu Ser Tyr Gly Ala Ile Gly Val
143          565          570          575
144 Ile Val Gly His Glu Phe Thr His Gly Phe Asp Asn Asn Gly Arg Lys
145          580          585          590
146 Tyr Asp Lys Asn Gly Asn Leu Asp Pro Trp Trp Ser Thr Glu Ser Glu
147          595          600          605
148 Glu Lys Phe Lys Glu Lys Thr Lys Cys Met Ile Asn Gln Tyr Ser Asn
149          610          615          620
150 Tyr Tyr Trp Lys Lys Ala Gly Leu Asn Val Lys Gly Lys Arg Thr Leu

```

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TIME: 20:03:19

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08102006\J588030.raw

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151 625          630          635          640
152 Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Arg Glu Ala Phe Arg Ala
153          645          650          655
154 Tyr Arg Lys Trp Ile Asn Asp Arg Arg Gln Gly Leu Glu Glu Pro Leu
155          660          665          670
156 Leu Pro Gly Ile Thr Phe Thr Asn Asn Gln Leu Phe Phe Leu Ser Tyr
157          675          680          685
158 Ala His Val Arg Cys Asn Ser Tyr Arg Pro Glu Ala Ala Arg Glu Gln
159          690          695          700
160 Val Gln Ile Gly Ala His Ser Pro Pro Gln Phe Arg Val Asn Gly Ala
161 705          710          715          720
162 Ile Ser Asn Phe Glu Phe Gln Lys Ala Phe Asn Cys Pro Pro Asn
163          725          730          735
164 Ser Thr Met Asn Arg Gly Met Asp Ser Cys Arg Leu Trp
165          740          745
167 <210> SEQ ID NO: 3
168 <211> LENGTH: 22
169 <212> TYPE: DNA
170 <213> ORGANISM: artificial sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: forward primer
175 <400> SEQUENCE: 3
176 tgagaaagcg attgaaaaag ca                                22
178 <210> SEQ ID NO: 4
179 <211> LENGTH: 16
180 <212> TYPE: DNA
181 <213> ORGANISM: artificial sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: reverse primer
186 <400> SEQUENCE: 4
187 gggccagcgg aaaggt                                16
189 <210> SEQ ID NO: 5
190 <211> LENGTH: 29
191 <212> TYPE: DNA
192 <213> ORGANISM: artificial sequence
194 <220> FEATURE:
195 <223> OTHER INFORMATION: probe
197 <400> SEQUENCE: 5
198 caagccactg ctacacatcc tacggcatt                    29

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/588,030

DATE: 08/10/2006

TIME: 20:03:20

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08102006\J588030.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

**Raw Sequence Listing before editing
(for reference only)**



IFWP

RAW SEQUENCE LISTING

DATE: 08/08/2006

PATENT APPLICATION: US/10/588,030

TIME: 09:18:48

Input Set : A:\004974.01208 sequence listing.txt

Output Set: N:\CRF4\08082006\J588030.raw

3 <110> APPLICANT: Bayer HealthCare AG
5 <120> TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
6 Phosphate Regulating Endopeptidase Homolog (PHEX)
8 <130> FILE REFERENCE: 004974.01208
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/588,030
C--> 10 <141> CURRENT FILING DATE: 2006-08-01
10 <160> NUMBER OF SEQ ID NOS: 5
12 <170> SOFTWARE: PatentIn version 3.2

ERRORED SEQUENCES

189 <210> SEQ ID NO: 5
190 <211> LENGTH: 29
191 <212> TYPE: DNA
192 <213> ORGANISM: artificial sequence
194 <220> FEATURE:
195 <223> OTHER INFORMATION: probe
197 <400> SEQUENCE: 5
E--> 198 caagccactg ctacacatcc tacggcatt

*Does Not Comply
Corrected Diskette Needed*

29[*1]

VERIFICATION SUMMARY

DATE: 08/08/2006

PATENT APPLICATION: US/10/588,030

TIME: 09:18:49

Input Set : A:\004974.01208 sequence listing.txt

Output Set: N:\CRF4\08082006\J588030.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:198 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:5
L:198 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:198 M:252 E: No. of Seq. differs, <211> LENGTH:Input:29 Found:32 SEQ:5